

SEQUENCE LISTING

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Eisenhaber, Frank  
Rea, Stephen

<120> Chromatin-Regulator Genes

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<140> US 09/589,892  
<141> 2000-06-09

<150> US 08/945,988  
<151> 1997-11-10

<150> PCT/EP96/01818  
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<151> 1995-05-10

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gag aag gga cca gtt tgt tgg cgg aag cgt gta aaa tca gag tac atg 161  
Glu Lys Gly Pro Val Cys Trp Arg Lys Arg Val Lys Ser Glu Tyr Met  
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cga ctg aga cag ctc aag agg ttc aga cga gct gat gaa gta aag agt 209  
Arg Leu Arg Gln Leu Lys Arg Phe Arg Arg Ala Asp Glu Val Lys Ser  
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Asn Gln Glu Trp Lys Gln Arg Arg Ile Gln Pro Val His Ile Leu Thr			
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Ser Val Ser Ser Leu Arg Gly Thr Arg Glu Cys Ser Val Thr Ser Asp			
75	80	85	
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Leu Asp Phe Pro Thr Gln Val Ile Pro Leu Lys Thr Leu Asn Ala Val			
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gct tca gta ccc ata atg tat tct tgg tct ccc cta cag cag aat ttt			449
Ala Ser Val Pro Ile Met Tyr Ser Trp Ser Pro Leu Gln Gln Asn Phe			
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atg gtg gaa gat gaa act gtt tta cat aac att cct tat atg gga gat			497
Met Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly Asp			
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Glu Val Leu Asp Gln Asp Gly Thr Phe Ile Glu Glu Leu Ile Lys Asn			
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Tyr Asp Gly Lys Val His Gly Asp Arg Glu Cys Gly Phe Ile Asn Asp			
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Glu Ile Phe Val Glu Leu Val Asn Ala Leu Gly Gln Tyr Asn Asp Asp			
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Glu Gln Gln Leu Pro Gly Ala Leu Pro Pro Glu Cys Thr Pro Asn Ile			
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Asp Gly Pro Asn Ala Lys Ser Val Gln Arg Glu Gln Ser Leu His Ser			
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ttt cat acg ctt ttc tgt agg cga tgt ttt aaa tat gac tgc ttc cta			977
Phe His Thr Leu Phe Cys Arg Arg Cys Phe Lys Tyr Asp Cys Phe Leu			
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gaa gca aat tct cgg tgt caa aca cca ata aag atg aag cca aat att Glu Ala Asn Ser Arg Cys Gln Thr Pro Ile Lys Met Lys Pro Asn Ile 410 415 420	1361
gaa cct cct gag aat gtg gag tgg agt ggt gct gaa gcc tca atg ttt Glu Pro Pro Glu Asn Val Glu Trp Ser Gly Ala Glu Ala Ser Met Phe 425 430 435 440	1409
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cca agg aaa aag aag agg aaa cac cgg ttg tgg gct gca cac tgc aga Pro Arg Lys Lys Arg Lys His Arg Leu Trp Ala Ala His Cys Arg 490 495 500	1601
aag ata cag ctg aaa aag gac ggc tcc tct aac cat gtt tac aac tat Lys Ile Gln Leu Lys Lys Asp Gly Ser Ser Asn His Val Tyr Asn Tyr 505 510 515 520	1649
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aag cag tgc ccg tgc tac ctg gct gtc cga gag tgt gac cct gac ctc Lys Gln Cys Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp Leu	570	575	580	1841
tgt ctt act tgt gga gcc gct gac cat tgg gac agt aaa aat gtg tcc Cys Leu Thr Cys Gly Ala Ala Asp His Trp Asp Ser Lys Asn Val Ser	585	590	595	1889
tgc aag aac tgc agt att cag cgg ggc tcc aaa aag cat cta ttg ctg Cys Lys Asn Cys Ser Ile Gln Arg Gly Ser Lys Lys His Leu Leu	605	610	615	1937
gca cca tct gac gtg gca ggc tgg ggg att ttt atc aaa gat cct gtg Ala Pro Ser Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro Val	620	625	630	1985
cag aaa aat gaa ttc atc tca gaa tac tgt gga gag att att tctcaa Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser Gln	635	640	645	2033
gat gaa gct gac aga aga ggg aaa gtg tat gat aaa tac atg tgc agc Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met Cys Ser	650	655	660	2081
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ggt aac aaa att cgt ttt gca aat cat tcg gta aat cca aac tgc tat Gly Asn Lys Ile Arg Phe Ala Asn His Ser Val Asn Pro Asn Cys Tyr	685	690	695	2177
gca aaa gtt atg atg gtt aac ggt gat cac agg ata ggt att ttt gcc Ala Lys Val Met Val Asn Gly Asp His Arg Ile Gly Ile Phe Ala	700	705	710	2225
aag aga gcc atc cag act ggc gaa gag ctg ttt ttt gat tac aga tac Lys Arg Ala Ile Gln Thr Gly Glu Glu Leu Phe Phe Asp Tyr Arg Tyr	715	720	725	2273
agc cag gct gat gcc ctg aag tat gtc ggc atc gaa aga gaa atg gaa Ser Gln Ala Asp Ala Leu Lys Tyr Val Gly Ile Glu Arg Glu Met Glu	730	735	740	2321
atc cct tga catctgctac ctcccccc tcctctgaaa cagctgcctt Ile Pro	745			2370
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Arg Glu Cys Ser Val Thr Ser Asp Leu Asp Phe Pro Thr Gln Val Ile  
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Trp Ser Pro Leu Gln Gln Asn Phe Met Val Glu Asp Glu Thr Val Leu  
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His Asn Ile Pro Tyr Met Gly Asp Glu Val Leu Asp Gln Asp Gly Thr  
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Arg Glu Cys Gly Phe Ile Asn Asp Glu Ile Phe Val Glu Leu Val Asn  
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Ala Leu Gly Gln Tyr Asn Asp Asp Asp Asp Asp Gly Asp Asp  
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Pro Glu Glu Arg Glu Glu Lys Gln Lys Asp Leu Glu Asp His Arg Asp  
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Gln Arg Glu Gln Ser Leu His Ser Phe His Thr Leu Phe Cys Arg Arg  
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Cys Phe Lys Tyr Asp Cys Phe Leu His Pro Phe His Ala Thr Pro Asn  
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Thr Tyr Lys Arg Lys Asn Thr Glu Thr Ala Leu Asp Asn Lys Pro Cys  
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Tyr Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys  
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Val Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp  
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His Ser Val Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Asn Gly  
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Asp His Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Thr Gly Glu  
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gac ctg tgc cgc ctg gcc aag ctc tcc tgc cct gcc ctc ggt atc tct 152  
Asp Leu Cys Arg Leu Ala Lys Leu Ser Cys Pro Ala Leu Gly Ile Ser  
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Lys Arg Asn Leu Tyr Asp Phe Glu Val Glu Tyr Leu Cys Asp Tyr Lys  
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Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp Arg Gly Tyr Pro  
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Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu Lys Cys Val Arg  
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atc ctc aag cag ttc cac aag gac tta gaa agg gag ctg ctc cgg cgg 344  
Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu Leu Leu Arg Arg  
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cac cac cgg tca aag acc ccc cgg cac ctg gac cca agc ttg gcc aac 392  
His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro Ser Leu Ala Asn  
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tac ctg gtg cag aag gcc aag cag agg cgg gcg ctc cgt cgc tgg gag 440  
Tyr Leu Val Gln Lys Ala Lys Gln Arg Arg Ala Leu Arg Arg Trp Glu  
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cag gag ctc aat gcc aag cgc agc cat ctg gga cgc atc act gta gag	488
Gln Glu Leu Asn Ala Lys Arg Ser His Leu Gly Arg Ile Thr Val Glu	
135 140 145	
aat gag gtg gac ctg gac ggc cct ccg cgg gcc ttc gtg tac atc aat	536
Asn Glu Val Asp Leu Asp Gly Pro Pro Arg Ala Phe Val Tyr Ile Asn	
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gag tac cgt gtt ggt gag ggc atc acc ctc aac cag gtg gct gtg ggc	584
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Cys Glu Cys Gln Asp Cys Leu Trp Ala Pro Thr Gly Gly Cys Cys Pro	
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Gly Tyr Asp Cys Pro Asn Arg Val Val Gln Lys Gly Ile Arg Tyr Asp	
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Leu Glu Lys Ile Arg Lys Asn Ser Phe Val Met Glu Tyr Val Gly Glu	
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Thr Val Asp Ala Ala Tyr Tyr Gly Asn Ile Ser His Phe Val Asn His	
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Cys Asp Tyr Lys Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp  
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Arg Gly Tyr Pro Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu  
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Lys Cys Val Arg Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu  
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Leu Leu Arg Arg His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro  
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Ile Thr Val Glu Asn Glu Val Asp Leu Asp Gly Pro Pro Arg Ala Phe  
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Gly Cys Cys Pro Gly Ala Ser Leu His Lys Phe Ala Tyr Asn Asp Gln  
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Gly Val Arg Thr Leu Glu Lys Ile Arg Lys Asn Ser Phe Val Met Glu  
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Glu Asp Val Tyr Thr Val Asp Ala Ala Tyr Tyr Gly Asn Ile Ser His  
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Arg Thr Ile Arg Ala Gly Glu Glu Leu Thr Phe Asp Tyr Asn Met Gln  
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Val Asp Pro Val Asp Met Glu Ser Thr Arg Met Asp Ser Asn Phe Gly  
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Leu Ala Gly Leu Pro Gly Ser Pro Lys Lys Arg Val Arg Ile Glu Cys  
385 390 395 400

Lys Cys Gly Thr Glu Ser Cys Arg Lys Tyr Leu Phe  
405 410

<210> 5  
<211> 489  
<212> DNA  
<213> Homo sapiens

<400> 5  
actcacctgt ggggcctcag agcactggga ctgcaagggtg gtttcctgtta aaaaactgcag 60  
catccagcgt ggacttaaga agcacctgct gctggcccccc tctgatgtgg ccggatgggg 120  
caccttcata aaggagtctg tgcagaagaa cgaattcatt tctgaatact gtggtgagct 180  
catctctcag gatgaggctg atcgacgcgg aaaggtctat gacaaataca tgtccagctt 240  
cctcttcaac ctcaataatg attttgttagt ggatgctact cgaaaaaggaa acaaaaattcg 300  
atttgcaaat cattcagtga atcccaactg ttatgccaaa ggtgagtcgg agtaacctgg 360

gaggtggggt ggggatgga tgcctttt ctgtgattc cattcggtt tgaacattt	420
ccttagctga gctatctttt gtccaaagat aatcatgatt aatatctggt atcattttag	480
ccccctctc	489
<210> 6	
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aattctcgag ctcgtcgaca	20
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<400> 7	
actgaattcg gctggggcat ctttcttaag g	31
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actctagaca atttccattt cacgctctat g	31
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<211> 30	
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<213> Drosophila melanogaster.	
<400> 9	
atatagtact tcaagtccat tcaaaagagg	30
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<211> 29	
<212> DNA	
<213> Drosophila melanogaster	
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ccaggtaccg ttggtgctgt ttaagaccg	29
<210> 11	
<211> 760	
<212> PRT	
<213> Drosophila melanogaster	
<400> 11	

Met Asn Ser Thr Lys Val Pro Pro Glu Trp Lys Arg Arg Val Lys Ser  
1 5 10 15

Glu Tyr Ile Lys Ile Arg Gln Gln Lys Arg Tyr Lys Arg Ala Asp Glu  
20 25 30

Ile Lys Glu Ala Trp Ile Arg Asn Trp Asp Glu His Asn His Asn Val  
35 40 45

Gln Asp Leu Tyr Cys Glu Ser Lys Val Trp Gln Ala Lys Pro Tyr Asp  
50 55 60

Pro Pro His Val Asp Cys Val Lys Arg Ala Glu Val Thr Ser Tyr Asn  
65 70 75 80

Gly Ile Pro Ser Gly Pro Gln Lys Val Pro Ile Cys Asx Ile Asn Ala  
85 90 95

Val Thr Pro Ile Pro Thr Met Tyr Thr Trp Ala Pro Thr Gln Gln Asn  
100 105 110

Phe Met Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly  
115 120 125

Asp Glu Val Leu Asp Lys Asp Gly Lys Phe Ile Glu Glu Leu Ile Lys  
130 135 140

Asn Tyr Asp Gly Lys Val His Gly Asp Lys Asp Pro Ser Phe Met Asp  
145 150 155 160

Asp Ala Ile Phe Val Glu Leu Val His Ala Leu Met Arg Ser Tyr Ser  
165 170 175

Lys Glu Leu Glu Glu Ala Ala Pro Ser Thr Ser Thr Ala Ile Lys Thr  
180 185 190

Glu Pro Leu Ala Lys Ser Lys Gln Gly Glu Asp Asp Gly Val Val Asp  
195 200 205

Val Asp Ala Asp Cys Glu Ser Pro Met Lys Leu Glu Lys Thr Glu Ser  
210 215 220

Lys Gly Asp Leu Thr Asp Val Glu Lys Lys Glu Thr Glu Glu Pro Val  
225 230 235 240

Glu Thr Glu Asp Ala Asp Val Lys Pro Ala Val Glu Glu Val Lys Asp  
245 250 255

Lys Leu Pro Phe Pro Ala Pro Ile Ile Phe Gln Ala Ile Ser Ala Asn  
260 265 270

Phe Pro Asp Lys Gly Thr Ala Gln Glu Leu Lys Glu Lys Tyr Ile Glu  
275 280 285

Leu Thr Glu His Gln Asp Pro Glu Arg Pro Gln Glu Cys Thr Pro Asn  
290 295 300

Ile Asp Gly Ile Lys Ala Glu Ser Val Ser Arg Glu Arg Thr Met His  
305 310 315 320

Ser Phe His Thr Leu Pro Cys Arg Arg Cys Phe Lys Tyr Asp Cys Phe  
325 330 335

Leu His Arg Leu Gln Gly His Ala Gly Pro Asn Leu Gln Lys Arg Arg  
340 345 350

Tyr Pro Glu Leu Lys Pro Phe Ala Glu Pro Cys Ser Asn Ser Cys Tyr  
355 360 365

Met Leu Ile Asp Gly Met Lys Glu Lys Leu Ala Ala Asp Ser Lys Thr  
370 375 380

Pro Pro Ile Asp Ser Cys Asn Glu Ala Ser Ser Glu Asp Ser Asn Asp  
385 390 395 400

Ser Asn Ser Gln Phe Ser Asn Lys Asp Phe Asn His Glu Asn Ser Lys  
405 410 415

Asp Asn Gly Leu Thr Val Asn Ser Ala Ala Val Ala Glu Ile Asn Ser  
420 425 430

Ile Met Ala Gly Met Met Asn Ile Thr Ser Thr Gln Cys Val Trp Thr  
435 440 445

Gly Ala Asp Gln Ala Leu Tyr Arg Val Leu His Lys Val Tyr Leu Lys  
450 455 460

Asn Tyr Cys Ala Ile Ala His Asn Met Leu Thr Lys Thr Cys Arg Gln  
465 470 475 480

Val Tyr Glu Phe Ala Gln Lys Glu Asp Ala Glu Ser Phe Ser Glu Asp  
485 490 495

Leu Arg Gln Asp Phe Thr Pro Pro Arg Lys Lys Lys Lys Gln Arg

500

505

510

Leu Trp Ser Leu His Cys Arg Lys Ile Gln Leu Lys Lys Asp Ser Ser  
515 520 525

Ser Asn His Val Tyr Asn Tyr Thr Arg Cys Asp His Pro Gly His Pro  
530 535 540

Cys Asp Met Asn Cys Ser Cys Ile Gln Thr Gln Asn Phe Cys Glu Lys  
545 550 555 560

Phe Cys Asn Cys Ser Ser Asp Cys Gln Asn Arg Phe Pro Gly Cys Arg  
565 570 575

Cys Lys Ala Gln Cys Asn Thr Lys Gln Cys Pro Cys Tyr Leu Ala Val  
580 585 590

Arg Glu Cys Asp Pro Asp Leu Cys Gln Ala Cys Gly Ala Asp Gln Phe  
595 600 605

Lys Leu Thr Lys Ile Thr Cys Lys Asn Val Cys Val Gln Arg Gly Leu  
610 615 620

His Lys His Leu Leu Met Ala Pro Ser Asp Ile Ala Gly Trp Gly Ile  
625 630 635 640

Phe Leu Lys Glu Gly Ala Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys  
645 650 655

Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr  
660 665 670

Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp Phe Val  
675 680 685

Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn His Ser  
690 695 700

Ile Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Thr Gly Asp His  
705 710 715 720

Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Pro Gly Glu Glu Leu  
725 730 735

Phe Phe Asp Tyr Arg Tyr Gly Pro Thr Glu Gln Leu Lys Phe Val Gly  
740 745 750

Ile Glu Arg Glu Met Glu Ile Val  
755                    760

<210> 12  
<211> 134  
<212> PRT  
<213> Homo sapiens  
  
<400> 12

Ser Pro Ile His Gly Arg Gly Leu Phe Cys Lys Arg Asn Ile Asp Ala  
1                    5                    10                    15

Gly Glu Met Val Ile Glu Tyr Ala Gly Asn Val Ile Arg Ser Ile Gln  
20                    25                    30

Thr Asp Lys Arg Glu Lys Tyr Tyr Asp Ser Lys Gly Ile Gly Cys Tyr  
35                    40                    45

Met Phe Arg Ile Asp Asp Ser Glu Val Val Asp Ala Thr Met His Gly  
50                    55                    60

Asn Arg Ala Arg Phe Ile Asn His Ser Cys Glu Pro Asn Cys Tyr Ser  
65                    70                    75                    80

Arg Val Ile Asn Ile Asp Gly Gln Lys His Ile Val Ile Phe Ala Met  
85                    90                    95

Arg Lys Ile Tyr Arg Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro  
100                    105                    110

Ile Glu Asp Ala Ser Asn Lys Leu Pro Cys Asn Cys Gly Ala Lys Lys  
115                    120                    125

Cys Arg Lys Phe Leu Asn  
130

<210> 13  
<211> 132  
<212> PRT  
<213> Drosophila melanogaster  
  
<400> 13

Ser His Ile His Gly Arg Gly Leu Tyr Cys Thr Lys Asp Ile Glu Ala  
1                    5                    10                    15

Gly Glu Met Val Ile Glu Tyr Ala Gly Glu Leu Ile Arg Ser Thr Leu  
20                    25                    30

Thr Asp Lys Arg Glu Arg Tyr Tyr Asp Ser Arg Gly Ile Gly Cys Tyr  
35 40 45

Met Phe Lys Ile Asp Asp Asn Leu Val Val Asp Ala Thr Met Arg Gly  
50 55 60

Asn Ala Ala Arg Phe Ile Asn His Cys Cys Glu Pro Asn Cys Tyr Ser  
65 70 75 80

Lys Val Val Asp Ile Leu Gly His Lys His Ile Ile Ile Phe Ala Val  
85 90 95

Arg Arg Ile Val Gln Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro  
100 105 110

Phe Glu Asp Glu Lys Ile Pro Cys Ser Cys Gly Ser Lys Arg Cys Arg  
115 120 125

Lys Tyr Leu Asn  
130

<210> 14  
<211> 133  
<212> PRT  
<213> *Caenorhabditis elegans*

<400> 14

Ser Arg Ile His Gly Trp Gly Leu Tyr Ala Met Glu Ser Ile Ala Pro  
1 5 10 15

Asp Glu Met Ile Val Glu Tyr Ile Gly Gln Thr Ile Arg Ser Leu Val  
20 25 30

Ala Glu Glu Arg Glu Lys Ala Tyr Glu Arg Arg Gly Ile Gly Ser Ser  
35 40 45

Tyr Leu Phe Arg Ile Asp Leu His His Val Ile Asp Ala Thr Lys Arg  
50 55 60

Gly Asn Phe Ala Arg Phe Ile Asn His Ser Cys Gln Pro Asn Cys Tyr  
65 70 75 80

Ala Lys Val Leu Thr Ile Glu Gly Glu Lys Arg Ile Val Ile Tyr Ser  
85 90 95

Arg Thr Ile Ile Lys Lys Gly Glu Glu Ile Thr Tyr Asp Tyr Lys Phe  
100 105 110

Pro Ile Glu Asp Asp Lys Ile Asp Cys Leu Cys Gly Ala Lys Thr Cys  
115 120 125

Arg Gly Tyr Leu Asn  
130

<210> 15  
<211> 136  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 15

Ser Ala Ile His Asn Trp Gly Leu Tyr Ala Leu Asp Ser Ile Ala Ala  
1 5 10 15

Lys Glu Met Ile Ile Glu Tyr Val Gly Glu Arg Ile Arg Gln Pro Val  
20 25 30

Ala Glu Met Arg Glu Lys Arg Tyr Leu Lys Asn Gly Ile Gly Ser Ser  
35 40 45

Tyr Leu Phe Arg Val Asp Glu Asn Thr Val Ile Asp Ala Thr Lys Lys  
50 55 60

Gly Gly Ile Ala Arg Phe Ile Asn His Cys Cys Asp Pro Asn Cys Thr  
65 70 75 80

Ala Lys Ile Ile Lys Val Gly Arg Arg Arg Ile Val Ile Tyr Ala  
85 90 95

Leu Arg Asp Ile Ala Ala Ser Glu Glu Leu Thr Tyr Asp Tyr Lys Phe  
100 105 110

Glu Arg Glu Lys Asp Asp Glu Glu Arg Leu Pro Cys Leu Cys Gly Ala  
115 120 125

Pro Asn Cys Lys Gly Phe Leu Asn  
130 135

<210> 16  
<211> 429  
<212> PRT  
<213> *Drosophila melanogaster*

<400> 16

Met Gly Val Ile Ala Lys Arg Pro Pro Lys Gly Glu Tyr Val Val Glu  
1 5 10 15

Arg Ile Glu Cys Val Glu Asn Asp Gln Tyr Gln Pro Val Phe Phe Val  
20 25 30

Lys Trp Leu Gly Tyr His Asp Ser Glu Asn Thr Trp Glu Ser Leu Ala  
35 40 45

Asn Val Ala Asp Cys Ala Glu Met Glu Lys Phe Val Glu Arg His Gln  
50 55 60

Gln Leu Tyr Glu Thr Tyr Ile Ala Lys Ile Thr Thr Glu Leu Glu Lys  
65 70 75 80

Gln Leu Glu Ala Leu Pro Leu Met Glu Asn Ile Thr Val Ala Glu Val  
85 90 95

Asp Ala Tyr Glu Pro Leu Asn Leu Gln Ile Asp Leu Ile Leu Ala  
100 105 110

Gln Tyr Arg Ala Ala Gly Ser Arg Ser Gln Arg Glu Pro Gln Lys Ile  
115 120 125

Gly Glu Arg Ala Leu Lys Ser Met Gln Ile Lys Arg Ala Gln Phe Val  
130 135 140

Arg Arg Lys Gln Leu Ala Asp Leu Ala Leu Phe Glu Lys Arg Met Asn  
145 150 155 160

His Val Glu Lys Pro Ser Pro Pro Ile Arg Val Glu Asn Asn Ile Asp  
165 170 175

Leu Asp Thr Ile Asp Ser Asn Phe Met Tyr Ile His Asp Asn Ile Ile  
180 185 190

Gly Lys Asp Val Pro Lys Pro Glu Ala Gly Ile Val Gly Cys Lys Cys  
195 200 205

Thr Glu Asp Thr Glu Glu Cys Thr Ala Ser Thr Lys Cys Cys Ala Arg  
210 215 220

Phe Ala Gly Glu Leu Phe Ala Tyr Glu Arg Ser Thr Arg Arg Leu Arg  
225 230 235 240

Leu Arg Pro Gly Ser Ala Ile Tyr Glu Cys Asn Ser Arg Cys Ser Cys  
245 250 255

Asp Ser Ser Cys Ser Asn Arg Leu Val Gln His Gly Arg Gln Val Pro  
260 265 270

Leu Val Leu Phe Lys Thr Ala Asn Gly Ser Gly Trp Gly Val Arg Ala  
275 280 285

Ala Thr Ala Leu Arg Lys Gly Glu Phe Val Cys Glu Tyr Ile Glu Glu  
290 295 300

Ile Ile Thr Ser Asp Glu Ala Asn Glu Arg Gly Lys Ala Tyr Asp Asp  
305 310 315 320

Asn Gly Arg Thr Tyr Leu Phe Asp Leu Asp Tyr Asn Thr Ala Gln Asp  
325 330 335

Ser Glu Tyr Thr Ile Asp Ala Ala Asn Tyr Gly Asn Ile Ser His Phe  
340 345 350

Ile Asn His Ser Cys Asp Pro Asn Leu Ala Val Phe Pro Cys Trp Ile  
355 360 365

Glu His Leu Asn Val Ala Leu Pro His Leu Val Phe Phe Thr Leu Arg  
370 375 380

Pro Ile Lys Ala Gly Glu Glu Leu Ser Phe Asp Tyr Ile Arg Ala Asp  
385 390 395 400

Asn Glu Asp Val Pro Tyr Glu Asn Leu Ser Thr Ala Val Arg Val Glu  
405 410 415

Cys Arg Cys Gly Arg Asp Asn Cys Arg Lys Val Leu Phe  
420 425

<210> 17  
<211> 166  
<212> PRT  
<213> Homo sapiens

<400> 17

Thr Ala Lys Met Gly Trp Gly Val Arg Ala Leu Gln Thr Ile Pro Gln  
1 5 10 15

Gly Thr Phe Ile Cys Glu Tyr Val Gly Glu Leu Ile Ser Asp Ala Glu  
20 25 30

Ala Asp Val Arg Glu Asp Asp Ser Tyr Leu Phe Asp Leu Asp Asn Lys  
35 40 45

Asp Gly Glu Val Tyr Cys Ile Asp Ala Arg Tyr Tyr Gly Asn Ile Ser  
50 55 60

Arg Phe Ile Asn His Leu Cys Asp Pro Asn Ile Ile Pro Val Arg Val  
65 70 75 80

Phe Met Leu His Gln Asp Leu Arg Phe Pro Arg Ile Ala Phe Phe Ser  
85 90 95

Ser Arg Asp Ile Arg Thr Gly Glu Glu Leu Gly Phe Asp Tyr Gly Asp  
100 105 110

Arg Phe Trp Asp Ile Lys Ser Lys Tyr Phe Thr Cys Gln Cys Gly Ser  
115 120 125

Glu Lys Cys Lys His Ser Ala Glu Ala Ile Ala Leu Glu Gln Ser Arg  
130 135 140

Leu Ala Arg Leu Asp Pro His Pro Glu Leu Leu Pro Glu Leu Gly Ser  
145 150 155 160

Leu Pro Pro Val Asn Thr  
165

<210> 18  
<211> 139  
<212> PRT  
<213> Homo sapiens

<400> 18

Thr Gln Asn Lys Gly Trp Gly Ile Arg Cys Leu Asp Asp Ile Ala Lys  
1 5 10 15

Gly Ser Phe Val Cys Ile Tyr Ala Gly Lys Ile Leu Thr Asp Asp Phe  
20 25 30

Ala Asp Lys Glu Gly Leu Glu Met Gly Asp Glu Tyr Phe Ala Asn Leu  
35 40 45

Asp His Ile Glu Ser Val Glu Tyr Ile Ile Asp Ala Lys Leu Glu Gly  
50 55 60

Asn Leu Gly Arg Tyr Leu Asn His Ser Cys Ser Pro Asn Leu Phe Val  
65 70 75 80

Gln Asn Val Phe Val Asp Thr His Asp Leu Arg Phe Pro Trp Val Ala  
85 90 95

Phe Phe Ala Ser Lys Arg Ile Arg Ala Gly Thr Glu Leu Thr Trp Asp  
100 105 110

Tyr Asn Tyr Glu Val Gly Ser Val Glu Gly Lys Glu Leu Leu Cys Cys  
115 120 125

Cys Gly Ala Ile Glu Cys Arg Gly Arg Leu Leu  
130 135

<210> 19  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 19

Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro  
1 5 10 15

Arg Lys Gln Leu  
20

<210> 20  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 20

Met Gly Pro Arg Arg Arg Ser Arg Lys Pro Glu Ala Pro Arg Arg Arg  
1 5 10 15

Ser Pro Ser Pro  
20

<210> 21  
<211> 20  
<212> PRT  
<213> Rattus sp.

<400> 21

Met Ser Ser Arg Gly Gly Lys Lys Ser Thr Lys Thr Ser Arg Ser  
1 5 10 15

Ala Lys Ala Gly  
20